



Category: Metagenomics

Salinity and macrophyte drive the biogeography of the sedimentary bacterial communities in a brackish water coastal lagoon

Pratiksha Behera¹, Sofia Mahapatra¹, Madhusmita Mohapatra¹, Ji Yoon Kim², Tapan K. Adhya³, Vishakha Raina³, Mrutyunjay Suar³, Ajit K. Pattnaik¹ and Gurdeep Rastogi¹

¹Wetland Research and Training Centre, Chilika Development Authority, Barkul, Balugaon 752030, Odisha, INDIA

²Department of Integrated Biological Science, Pusan National University, Geumjeong-gu 46241, Busan, SOUTH KOREA

³School of Biotechnology, KIIT University, Patia, Bhubaneswar 751024, Odisha, INDIA

Presenting author: pratiksha.behera23@gmail.com

Abstract

Coastal lagoons are represented by steep gradients in physical, chemical, and biological parameters and are regarded as one of the most productive ecosystems in the world. These lagoons are at an intermediate position between the freshwater and marine water systems. Huge amount of influx of organic matter and nutrient load with the freshwater inputs can be seen in such lagoons. The increased influx of organic matter and nutrients fuel in the lagoon increases the chance of eutrophication. The sedimentary microbial communities play an important role in preventing eutrophication by supporting a diverse assemblage of aerobic and anaerobic microbial communities. Considering the importance of sedimentary bacterial communities, numerous studies have investigated their ecological roles and biogeographical patterns in a variety of aquatic ecosystems. Compared to the marine and freshwater ecosystems, estuarine coastal lagoons are highly dynamic, still are poorly understood with respect to their sedimentary communities. Our hypothesis was that bacterial communities would exhibit biogeographical patterns which would be strongly associated with the biotic and abiotic factors. Using Illumina sequencing of the 16S rRNA genes from bulk surface sediments, we investigated the sedimentary bacterial communities, their spatiotemporal distribution, and compared them with the rhizosphere sediment communities of an exotic weed; *P. karka* and a native seagrass species; *H. uninervis* in a brackish water estuarine lagoon, Chilika (India). Comparison of bacterial communities with the environmental factor was done using Redundancy analysis. Spatiotemporal patterns in bacterial communities were linked to specific biotic factors (e.g., presence and type of macrophyte) and abiotic factors (e.g., salinity) that drove the community composition. Comparative assessment of communities highlighted bacterial lineages that were responsible for segregating the sediment communities over distinct salinity regimes, seasons, locations, and presence and type of macrophytes. Several bacterial taxa were specific to one of these ecological factors suggesting that species-sorting processes drive specific biogeographical patterns in the bacterial populations. Overall, this study provides a comprehensive understanding of the spatiotemporal dynamics and functionality of sedimentary bacterial communities in a tropical brackish water coastal lagoon and highlighted the role of biotic and abiotic factors in generating the biogeographical patterns in the bacterial communities.

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